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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/037,860

DATE: 01/19/2002

TIME: 10:55:53

Input Set : A:\2581.1004-004 Sequence Listing.txt

Output Set: N:\CRF3\01192002\J037860.raw

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APR 01 2002

TECH CENTER 1600/2900

4 <110> APPLICANT: Jerome B. Posner
 5 Josep O. Dalmau
 6 Myrna R. Rosenfeld
 8 <120> TITLE OF INVENTION: Ma FAMILY POLYPEPTIDES AND ANTI-Ma
 9 ANTIBODIES
 11 <130> FILE REFERENCE: 2581.1004-004
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/037,860
 C--> 13 <141> CURRENT FILING DATE: 2001-01-04
 13 <150> PRIOR APPLICATION NUMBER: 09/189,527
 14 <151> PRIOR FILING DATE: 1998-11-10
 16 <160> NUMBER OF SEQ ID NOS: 14
 18 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 18
 22 <212> TYPE: DNA
 23 <213> ORGANISM: homo sapiens
 25 <400> SEQUENCE: 1
 26 gaaacccaag gacacggg
 28 <210> SEQ ID NO: 2
 29 <211> LENGTH: 19
 30 <212> TYPE: DNA
 31 <213> ORGANISM: homo sapiens
 33 <400> SEQUENCE: 2
 34 gtctttgcgg atgtccacg
 36 <210> SEQ ID NO: 3
 37 <211> LENGTH: 2139
 38 <212> TYPE: DNA
 39 <213> ORGANISM: homo sapiens
 41 <220> FEATURE:
 42 <221> NAME/KEY: CDS
 43 <222> LOCATION: (272)...(1258)
 45 <221> NAME/KEY: misc_feature
 46 <222> LOCATION: (1)...(2139)
 47 <223> OTHER INFORMATION: n = A, T, C or G
 49 <221> NAME/KEY: misc_feature
 50 <222> LOCATION: 1699
 51 <223> OTHER INFORMATION: n = A,T,C or G
 53 <400> SEQUENCE: 3
 54 cgaggagcga cggccggacc cagacccaga cgcaagatgg cgacggccgc gtgactgcct 60
 55 cagcgtcccc gagctcggct ccgagtgcac ctacggactg actgtggggg cagagaaggg 120
 56 cgaatcagg actctgtctt tgtaatcgt gactgcatga aggtcgccct cctcgggcct 180
 57 acttggtggg agtgtctggt attgttctaa ggccaggagc acggtgagcc acagtctgtt 240
 58 ggtagaattt ggcgtcttga tagttgagaa a atg gcg atg aca ctg ttg gaa 292

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59                               Met Ala Met Thr Leu Leu Glu
60                               1           5
62 gac tgg tgc cgg ggg atg gat gtg aac tcc cag aga act ctg tta gtc 340
63 Asp Trp Cys Arg Gly Met Asp Val Asn Ser Gln Arg Thr Leu Leu Val
64           10           15           20
66 tgg ggc atc cca gtg aac tgt gat gag gct gaa atc gaa gag acc ctc 388
67 Trp Gly Ile Pro Val Asn Cys Asp Glu Ala Glu Ile Glu Glu Thr Leu
68           25           30           35
70 cag gct gcg atg ccc cag gtc tcc tac cga atg ctt ggg aga atg ttc 436
71 Gln Ala Ala Met Pro Gln Val Ser Tyr Arg Met Leu Gly Arg Met Phe
72 40           45           50           55
74 tgg agg gaa gaa aat gcg aaa gca gcc tta tta gag ctc act ggc gct 484
75 Trp Arg Glu Glu Asn Ala Lys Ala Ala Leu Leu Glu Leu Thr Gly Ala
76           60           65           70
78 gta gat tac gcc gcg atc ccc agg gag atg ccg ggc aaa gga ggg gtc 532
79 Val Asp Tyr Ala Ala Ile Pro Arg Glu Met Pro Gly Lys Gly Gly Val
80           75           80           85
82 tgg aaa gtg tta ttt aag ccc cca act tct gat gct gaa ttt tta gaa 580
83 Trp Lys Val Leu Phe Lys Pro Pro Thr Ser Asp Ala Glu Phe Leu Glu
84           90           95           100
86 aga ttg cac ctc ttc cta gct aga gag ggg tgg acc gtg caa gat gtt 628
87 Arg Leu His Leu Phe Leu Ala Arg Glu Gly Trp Thr Val Gln Asp Val
88 105           110           115
90 gcc cgt gtc ctt ggg ttt cag aac cct act ccg acc ccg ggc cca gag 676
91 Ala Arg Val Leu Gly Phe Gln Asn Pro Thr Pro Thr Pro Gly Pro Glu
92 120           125           130           135
94 atg cca gca gag atg cta aac tat att ttg gat aat gtt att cag cct 724
95 Met Pro Ala Glu Met Leu Asn Tyr Ile Leu Asp Asn Val Ile Gln Pro
96           140           145           150
98 ctt gtt gag tcc ata tgg tac aag agg ctg aca ctt ttc tcg ggg aag 772
99 Leu Val Glu Ser Ile Trp Tyr Lys Arg Leu Thr Leu Phe Ser Gly Lys
100           155           160           165
102 gga cat ccc agg gcc tgg aga gga aac ttt gat ccc tgg ctg gag cac 820
103 Gly His Pro Arg Ala Trp Arg Gly Asn Phe Asp Pro Trp Leu Glu His
104           170           175           180
106 act aat gag gtc cta gag gag tgg cag gtg tcc gat gta gaa aag agg 868
107 Thr Asn Glu Val Leu Glu Glu Trp Gln Val Ser Asp Val Glu Lys Arg
108 185           190           195
110 cgg cgg ttg atg gag agt ctt aga ggc ccc gcc gct gat gtt att cgc 916
111 Arg Arg Leu Met Glu Ser Leu Arg Gly Pro Ala Ala Asp Val Ile Arg
112 200           205           210           215
114 atc ctt aag tcc aac aac ccc gcg ata acc act gcc gaa tgc ctg aag 964
115 Ile Leu Lys Ser Asn Asn Pro Ala Ile Thr Thr Ala Glu Cys Leu Lys
116           220           225           230
118 gcg ctt gag cag gtg ttt ggg agc gtt gag agc tct agg gat gcc cag 1012
119 Ala Leu Glu Gln Val Phe Gly Ser Val Glu Ser Ser Arg Asp Ala Gln
120           235           240           245
122 atc aaa ttt ctg aac act tat cag aac ccg gga gaa aaa ttg tct gct 1060
123 Ile Lys Phe Leu Asn Thr Tyr Gln Asn Pro Gly Glu Lys Leu Ser Ala

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124          250          255          260
126 tat gtc att cgt ctg gag cct ctg cta cag aag gtg gta gag aag ggg 1108
127 Tyr Val Ile Arg Leu Glu Pro Leu Leu Gln Lys Val Val Glu Lys Gly
128          265          270          275
130 gcc att gat aaa gat aat gtg aac cag gcc cgc cta gag cag gtc att 1156
131 Ala Ile Asp Lys Asp Asn Val Asn Gln Ala Arg Leu Glu Gln Val Ile
132 280          285          290          295
134 gcc ggg gcc aac cac agc ggg gcc atc cga agg cag ctg tgg ctt acc 1204
135 Ala Gly Ala Asn His Ser Gly Ala Ile Arg Arg Gln Leu Trp Leu Thr
136          300          305          310
138 ggg gct ggg gaa ggg cca ggc ccc aaa cct ctt tca gtt gct ggt gca 1252
139 Gly Ala Gly Glu Gly Pro Gly Pro Lys Pro Leu Ser Val Ala Gly Ala
140          315          320          325
142 gat ccg tgaggaggaa gccagggag gaggaggagg aggctgaggc cacccttctg 1308
143 Asp Pro
146 cagttaggcc tggaaggcca cttctgagtg ccaggaaagg cagctttagt gcagacctag 1368
147 atcacagcta cttttcttgt cctgtgggg ttttacagat gtgtctctga gtagtaaagg 1428
148 cttagccttg ttctgttttg ttgttttttg gaggggaagg ttagtcaggc ctgagtattc 1488
149 atgtaacatt ctaaaattgt gccagcgagc accgtgaacg actgcaatgc aagcgggtct 1548
150 tgctggctaa aatgcccagg taaaggggtg gttggacaca gcgcttagtg cagctgtca 1608
151 tcatggacat cataatcagt tgtgaaaaac acgcgaacct atgacacttc ttattccaca 1668
152 ctgaatgtga aattgcatgt tcagatgttt nactacgagg cctggctcac aggaagtgtt 1728
153 cagtaaaagt atgcactggt agattactga taacgcggat agatttttgt ttaccataaa 1788
154 ttgttccaga tttatatata tggaaggaag tgtgcattta ttagctatta ctcaacttta 1848
155 caatgcaaac atcttatttc tcatttttaa acatgtcgac cagtttaatt gaaaagtatt 1908
156 ctgagactgc aaaatggggt gttaaaaaat actgcagtta cggagctgtg taaaccagtt 1968
157 tctcattgca taagatacag atgtaaattg catggagagg ttgatatgca cctgtacagt 2028
158 aattcactcc ccatttcac ttctttgtca gagaatagtt cttgttcata ctgagtgttc 2088
159 taaatttgaa gttatatata caaattaaaa tattttaaaa aaaaaaaaaa g 2139
161 <210> SEQ ID NO: 4
162 <211> LENGTH: 329
163 <212> TYPE: PRT
164 <213> ORGANISM: homo sapiens
166 <400> SEQUENCE: 4
167 Met Ala Met Thr Leu Leu Glu Asp Trp Cys Arg Gly Met Asp Val Asn
168 1          5          10          15
169 Ser Gln Arg Thr Leu Leu Val Trp Gly Ile Pro Val Asn Cys Asp Glu
170          20          25          30
171 Ala Glu Ile Glu Glu Thr Leu Gln Ala Ala Met Pro Gln Val Ser Tyr
172          35          40          45
173 Arg Met Leu Gly Arg Met Phe Trp Arg Glu Glu Asn Ala Lys Ala Ala
174          50          55          60
175 Leu Leu Glu Leu Thr Gly Ala Val Asp Tyr Ala Ala Ile Pro Arg Glu
176 65          70          75          80
177 Met Pro Gly Lys Gly Gly Val Trp Lys Val Leu Phe Lys Pro Pro Thr
178          85          90          95
179 Ser Asp Ala Glu Phe Leu Glu Arg Leu His Leu Phe Leu Ala Arg Glu
180          100          105          110
181 Gly Trp Thr Val Gln Asp Val Ala Arg Val Leu Gly Phe Gln Asn Pro

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182          115          120          125
183 Thr Pro Thr Pro Gly Pro Glu Met Pro Ala Glu Met Leu Asn Tyr Ile
184          130          135          140
185 Leu Asp Asn Val Ile Gln Pro Leu Val Glu Ser Ile Trp Tyr Lys Arg
186 145          150          155          160
187 Leu Thr Leu Phe Ser Gly Lys Gly His Pro Arg Ala Trp Arg Gly Asn
188          165          170          175
189 Phe Asp Pro Trp Leu Glu His Thr Asn Glu Val Leu Glu Glu Trp Gln
190          180          185          190
191 Val Ser Asp Val Glu Lys Arg Arg Arg Leu Met Glu Ser Leu Arg Gly
192          195          200          205
193 Pro Ala Ala Asp Val Ile Arg Ile Leu Lys Ser Asn Asn Pro Ala Ile
194          210          215          220
195 Thr Thr Ala Glu Cys Leu Lys Ala Leu Glu Gln Val Phe Gly Ser Val
196 225          230          235          240
197 Glu Ser Ser Arg Asp Ala Gln Ile Lys Phe Leu Asn Thr Tyr Gln Asn
198          245          250          255
199 Pro Gly Glu Lys Leu Ser Ala Tyr Val Ile Arg Leu Glu Pro Leu Leu
200          260          265          270
201 Gln Lys Val Val Glu Lys Gly Ala Ile Asp Lys Asp Asn Val Asn Gln
202          275          280          285
203 Ala Arg Leu Glu Gln Val Ile Ala Gly Ala Asn His Ser Gly Ala Ile
204          290          295          300
205 Arg Arg Gln Leu Trp Leu Thr Gly Ala Gly Glu Gly Pro Gly Pro Lys
206 305          310          315          320
207 Pro Leu Ser Val Ala Gly Ala Asp Pro
208          325
211 <210> SEQ ID NO: 5
212 <211> LENGTH: 18
213 <212> TYPE: DNA
214 <213> ORGANISM: homo sapiens
216 <400> SEQUENCE: 5
217 gqqaatggcc gagacatc 18
219 <210> SEQ ID NO: 6
220 <211> LENGTH: 615
221 <212> TYPE: DNA
222 <213> ORGANISM: homo sapiens
224 <220> FEATURE:
225 <221> NAME/KEY: CDS
226 <222> LOCATION: (1)...(585)
228 <400> SEQUENCE: 6
229 ccc ctg gca ctg tta gag gac tgg tgc agg ata atg agt gtg gat gag 48
230 Pro Leu Ala Leu Leu Glu Asp Trp Cys Arg Ile Met Ser Val Asp Glu
231 1          5          10          15
233 cag aag tca ctg atg gtt acg ggg ata ccg gcg gac ttt gag gag gct 96
234 Gln Lys Ser Leu Met Val Thr Gly Ile Pro Ala Asp Phe Glu Glu Ala
235          20          25          30
237 gag att cag gag gtc ctt cag gag act tta aag tct ctg ggc agg tat 144
238 Glu Ile Gln Glu Val Leu Gln Glu Thr Leu Lys Ser Leu Gly Arg Tyr

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```

239          35          40          45
241 aga ctg ctt ggc aag ata ttc cgg aag cag gag aat gcc aat gct gtc 192
242 Arg Leu Leu Gly Lys Ile Phe Arg Lys Gln Glu Asn Ala Asn Ala Val
243          50          55          60
245 tta cta gag ctt ctg gaa gat act gat gtc tcg gcc att ccc agt gag 240
246 Leu Leu Glu Leu Leu Glu Asp Thr Asp Val Ser Ala Ile Pro Ser Glu
247 65          70          75          80
249 gtc cag gga aag ggg ggt gtc tgg aaa gtg atc ttt aag acc cct aat 288
250 Val Gln Gly Lys Gly Gly Val Trp Lys Val Ile Phe Lys Thr Pro Asn
251          85          90          95
253 cag gac act gag ttt ctt gaa aga ttg aac ctg ttt cta gaa aaa gag 336
254 Gln Asp Thr Glu Phe Leu Glu Arg Leu Asn Leu Phe Leu Glu Lys Glu
255          100          105          110
257 ggg cag acg gtc tcg ggt atg ttt cga gcc ctg ggg cag gag gcg ttg 384
258 Gly Gln Thr Val Ser Gly Met Phe Arg Ala Leu Gly Gln Glu Ala Leu
259          115          120          125
261 tct cca gcc aca gtg ccc tgc atc tca cca gaa tta ctg gcc cat ttg 432
262 Ser Pro Ala Thr Val Pro Cys Ile Ser Pro Glu Leu Leu Ala His Leu
263          130          135          140
265 ttg gga cag gca atg gca cat gcg cct cag ccc ctg cta ccc atg aga 480
266 Leu Gly Gln Ala Met Ala His Ala Pro Gln Pro Leu Leu Pro Met Arg
267          145          150          155          160
269 tac cgg aaa ctg cga gta ttc tca ggg agt gct gtc cca gcc cca gag 528
270 Tyr Arg Lys Leu Arg Val Phe Ser Gly Ser Ala Val Pro Ala Pro Glu
271          165          170          175
273 gaa gag tcc ttt gag gtc tgg ttg gaa cag gcc acg gag ata gtc aaa 576
274 Glu Glu Ser Phe Glu Val Trp Leu Glu Gln Ala Thr Glu Ile Val Lys
275          180          185          190
277 gag tgg cct tgaacacaac caaaaaaaaaa aaaaaaaaaag 615
278 Glu Trp Pro
279          195
282 <210> SEQ ID NO: 7
283 <211> LENGTH: 195
284 <212> TYPE: PRT
285 <213> ORGANISM: homo sapiens
287 <400> SEQUENCE: 7
288 Pro Leu Ala Leu Leu Glu Asp Trp Cys Arg Ile Met Ser Val Asp Glu
289 1          5          10          15
290 Gln Lys Ser Leu Met Val Thr Gly Ile Pro Ala Asp Phe Glu Glu Ala
291          20          25          30
292 Glu Ile Gln Glu Val Leu Gln Glu Thr Leu Lys Ser Leu Gly Arg Tyr
293          35          40          45
294 Arg Leu Leu Gly Lys Ile Phe Arg Lys Gln Glu Asn Ala Asn Ala Val
295          50          55          60
296 Leu Leu Glu Leu Leu Glu Asp Thr Asp Val Ser Ala Ile Pro Ser Glu
297 65          70          75          80
298 Val Gln Gly Lys Gly Gly Val Trp Lys Val Ile Phe Lys Thr Pro Asn
299          85          90          95
300 Gln Asp Thr Glu Phe Leu Glu Arg Leu Asn Leu Phe Leu Glu Lys Glu

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VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:152 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:679 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:680 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12